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Application Serial Number: 09/236, 995A

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TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

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The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2Kcompliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

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ERROR DETECTED SUGGESTED CORRECTION

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RAW SEQUENCE LISTING PATENT APPLICATION: US-09/236,995A DATE: 11/01/2000 TIME: 13:18:34

input Set : A:\Polyadpl.app
Output Set: N:\CRF3\11012000\1236995A.raw 3 <110> APPLICANT: Mahajan, Pramod B. 6 <120> TITLE OF INVENTION: Poly ADP-Ribose Polymerase Gene and its Uses 8 <130> FILE REFERENCE: 5718-34, 035718-174234 10 <140> CURRENT APPLICATION NUMBER: 09/236,395A 11 <141> CURRENT FILING DATE: 1999-01-26 13 <150> PRIOR APPLICATION NUMBER: 60/072,785 14 <151> PRIOR FILING DATE: 1998-01-27 16 < 169 > NUMBER OF SEQ TO NOS: 518 <170> SOFTWARE: Patentin Ver. 2.1 20 <210> SEQ ID NO: 1 21 <211> LENGTH: 2949 22 <212> TYPE: DNA 23 <213> ORGANISM: Zea mays 25 <220> FEATURE: 26 <221> NAME/KEY: CDS 27 <222> LOCATION: (1)..(2949) 29 <220> FEATURE: 30 <221> NAME/KEY: misc_feature 31 <.222> LOCATION: () --) 32 <223> OTHER INFORMATION: 6%A, T. C. or G 34 <220> FEATURE:

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37 <223> OTHER INFORMATION: Naa-unknown

RAW SEQUENCE LISTING PATENT APPLICATION: US/09/236,995A TIME: 13:18:34

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W>	166 168 169 170 172 173 174 175 177 178 180 181 182 184	gra Xaa cac His Ga: Asp 945 gau Giu	tgg Trp nag Xaa 730 qqq Oly	gaa Glu 515 gtg Val Left Ser at L	tgy Cys Laq Cys Taq Glu qqa Gly	cat His aca Thr Equ Cys uqu Gly 565 aca	ata Ile ggc Gly tac Tyr 550 caa Gln	caa Gln tac Tyr 535 qta val aaa Lys	tgc Cys 520 tat Tyr crt. Phe	gta val cgt Arg gaq Glu	ctt Leu ctc Leu aag Lys gag Glu 570	aaa Lys cag Gln tug Trp 555 atg Met	cat His atc Ile 540 gga Gly tca Ser	gtt Val 525 att Ile cgg Arg aaa Lys	gaa Glu gtt val act Thr	acc Thr cag Gln qgq Gl; qaq Glu 575 t;da Ser	gat Asp aqt Sor 560 qca Ala	1632 1686 1728
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DATE: 11/01/2000 TIME: 13:18:34

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265 Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp Lys Pro Pro
266 900 905 910
268 aga ggg aag cat tcg acc aag gga tta ggc aaa acc gtg cca ctg gag 269 Arg Cly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu Glu 270 915 920 925 272 tea gag tit gtg aag tyg agg gat gat gte gta gtt cee tge gge aag 273 Ser Glu Phe Val Lys Trp Arg Asp Val Val Val Pro Cys Gly Lys 940 935 274 930 276 deg gtg oca tea fea att agg age tet gaa ete ath tac aat gag tac 277 Pro Val Pro Ser Ser ite Arg Ser Ser Glu Leu Met Tyr Ash Glu Tyr 950 955 280 ate gto tac and how too day gty and aty day the tig dig may gig 281 lle Vai Tyr Asn Thr Ser Gin Vai Lys Met Gin Phe Leu Leu Lys Vai 282 955 970 975 284 cgt ttc cat cac aug nyg tag 285 Arg Phe His His Lys Arg 286 980 289 (210> SEQ ID NO: 2 290 <211> LENGTH: 982 -291 <212> TYPE: PRT 292 <213> ORGANISM: Zea mays 294 <400> SEQUENCE: 2 295 Met Ala Ala Pro Pro Lys Ala Trp Lys Ala Glu Tyr Ala Lys Ser Gl $_2$ 296 $_{-1}$. 5 $_{-10}$ 10 $_{-15}$ 297 Arg Ala Ser Cys Lys Ser Cys Arg Ser Pio Tle Ala Lys Asp Glu Lou 298 \pm - 20 - 25 - 30 299 Arg Leu Gly Lys Met Vol Gli Ala Ser Gli Phe Asp Gly Phe Met 1900 300 -35 -40 -45301 Met. Trp Ash His Ala Arg Cys lle Phe Ser Lys Lys Ash Gln He Lys 302-50 , 55-60303 Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Glu 304 -65 70 -75 -85304 65 305 Glu Lys He Arg Ash Fyr Val Gly Ser Ala Ser Ala Gly Thr Set Ser 306 90 95 307 Thr Aia Ala Pro Pro Glu Lys Cys Thr 11e Glu Ile Ala Pro Ser Aia 308 100 165 110 309 Arg Thr Ser Cys.Arg Arg Cys Ser Glu Lys IIe Thr Lys Gly Ser Val. 310 115 120 125 311 Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly 11e Pro Trp 312 130 135 140 313 Tyr His Ala Asu Cys the Phe Glu Val Ser Pro Ser Ala Thr Val Glu 314 145 150 150 160
 315 Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Ard Thr Met.

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 317 Len Asp Len Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly

 318
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 319 Ser Lys Arg Lys Lys Ser Glu Ash Asp Tle Asp Ser Tyr Lys Ser Ala 195 200

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			<u>~~</u>	Val	Cys			535					340				
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	G	lu			Gly	565					2/0					5,5	
	I	le	Lys	Glu	Phe	Lys	Arg	Leu	Phe	Leu 585	Glu	Lys	Thr	Gly	Asn 590	Ser	Trp
				EOE	580 Glu				600	Phe				003			
			C10	Leu	Asp			615					020				
	_	2.0	Ile		Glu		ครก					033					
	M	ſet			Leu	615	Asn				บอง					7	
				1 .) Asn 660	Met	Ser			りりつ						_	
				<i>C</i> 75	Xaa	Gly			คหบ	Leu	Thr			-000			Phe
	C	Glu			Arg	Xaa	Ser	Ser 695	Thr	Gly	Leu	Xaa)Glu 700	Lys	Ala	Xaa	Leu
				Xaa	Xaa	Xaa	Xaa -710	Phe	Ser	Leu	Leu	Ser 715	Leu	Leu	Phe	Ile	Leu 720
	:	705 Ile	Leu	Tyr	Gly	Met	Arg	Met	Ile	Ser	Tyr	Ser	Lys	Ala	Lys	Met 735	Leu
	(Glu	Ala	Leu) Ile	Glu	Ile	Ala 745	730 Ser	Lys		Val	Gly 750	Phe	Asp
	:	Ser	Asp			Glu	ı Ser	Leu	Asp 760	Asp	Lys	туг	Met	Lys 765	Leu	His	Cys
		Asp			r Pro	Lev	ı Ala	His 775	Asp	Ser	Glu	ı Asp	780	Lys	Leu	Ile	Glu
				Lev	ı Lev	ı Ası	n Thi 790	His	Ala	Pro	Th:	r His	Lys	s Asp	Trp	Sei	Leu 800
		785 Glu	Lei	ı Glı	u Glu	y Vai 80	l Phe	e Sei	Lev	ı Asp	Arg 810	g Asp	Gl3	y Glu	ı Lev	Asr 815	Lys
					821	r Ly:	s Ası			823	s Ası	n Ly:			031	,) His
				83	g Lei	u Th			841	1 G1:	y Il			04)		u Arg
		Ile	Ala 850	a Pr	o Pr	o Gl	u Al	a Pro 85	o Vai	l Th	r Gl	у Ту	86	t Pho	e Gl	y Ly	s Gly

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item 10
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Sheet

Input Set : A:\Polyadpl.app Output Set: N:\CRF3\11012000\1236995A.raw L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 L:169 M:341 W: (46) "n" or "xaa" used, for sso in 1 L:172 M:341 W: (46) "n" or "xaa" used for so in 1 L:173 M:341 W: (46) "n" or "xaa" used for sco in 1 L:205 M:341 W: (46) "n" or "xaa" used for sso in 1 L:209 M:341 W: (46) "n" or "Xaa" used, for SEO_ID#:1. L:212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 L:213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 L:217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 L:355 M:258 W: Mandatory Feature missing, <220> not found for SEO 1D#:2 L:355 M:258 W: Mandatory Feature missing, <221> not found for SEO 1D*:2 L:355 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2 L:355 M:258 W: Mandatory Feature missing, <223> not found for SEQ 1D::2 L:355 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEO 1D#:2 L:357 M:258 W: Mandatory Feature missing, <220> not found for SEO 1D*:2 L:357 M:258 W: Mandatory Feature missing, <221> not found for SEQ 1Dw:2 L:357 M:258 W: Mandatory Feature missing, <222> not found for SEQ 1D#:2 L:357 M:258 W: Mandatory Feature missing, <223> not found for SEO ID*:2 M:340 Repeated in SeqNo=2 L:359 M:258 W: Handatory Feature missing, <220> not found for SEO ID::2 L:359 M:258 W: Mandatory Feature missing, <221> not found for SEG Iffv:2 L:359 M:258 W: Mandatory Feature missing, <222> not found for SEO 10%:2 L:359 M:258 W: Mandatory Feature missing, <223> not found for SEQ IDE:3 L:361 M:255 W: Mandatory Feature missing, <220> not found for SEO TD::2 L:361 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID::2 L:361 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID::2 L:361 M:258 W: Mandatory Feature missing, <223> not found for SEO ffm:2 L:377 M:258 W: Mandatory Feature missing, <220> not found for SEQ 1D :2 L:377 H:258 W: Mandatory Peature missing. <221> not found for SEQ TU-:2 E:377 M:258 W: Mandatory Feature missing, <222> not found for SEO (De:2 L:377 M:258 W: Mandatory Feature missing, <223> not found for SFQ H::2 L:379 M:058 W: Mandatory Feature missing, <220> not found for SEg to .2 L:379 H:258 W: Mandatory Posture missing, <221> not found for SEO (D):2 L:379 H:258 W: Handatory Feature missing, <222> not found for SEO He :2 L:379 M:258 W: Mandatory Feature missing, (223> not found for SEO HDr a 1:381 M:258 W: Handatory Feature missing, <220> not found for SEQ (D).2 L:381 M:25% W: Mandatory Peature missing, <221> not found for SEQ TO :2 L:381 M:258 W: Mandatory Feature missing, <222> not found for SEO TUV:2 L:381 M:259 W: Mandatory Feature missing, <223> not found for SEG FF-:2 L:383 M:258 W: Mandatory Feature missing, <220> not found for SEO Her:2

L:383 H:258 W: Mandatory Feature missing, <2215 not found for SEQ $10^{\pm}:2$ L:383 H:258 W: Handatory Feature missing, <2225 not found for SEQ $10^{\pm}:2$ L:383 M:255 W: Mandatory Feature missing, <2235 not found for SEQ $10^{\pm}:2$